



<110> The General Hospital Corporation

<120> Rapid Immunoselection Cloning Method

<130> 11-88L

<140> US 09/836,544

<141> 2001-04-17

<150> US 07/983,647

<151> 1992-12-01

<150> US 07/553,759

<151> 1990-07-13

<150> US 07/498,809

<151> 1990-03-23

<150> US 07/379,076

<151> 1989-07-13

<150> US 07/160,416

<151> 1988-02-25

<160> 37

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Nucleotide sequence of expression vector, piH3

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atactgtcct tcttagtgttag ccgtagttag gccaccactt caagaactct gtagcaccgc 180

ctacataacct cgctctgcta atcctgttac cagtggtgc tgccagtggc gataagtcgt 240

gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg tcgggctgaa 300

cgggggggttc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa ctgagatacc 360

tacagcgtga gctatgagaa agcgccacgc ttcccgaaagg gagaaaggcg gacaggtatc 420

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RECEIVED  
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TECH CENTER 1600/2900

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ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc 96  
Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala  
15 20 25 30  
ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144  
Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro  
35 40 45  
agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act 192  
Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr  
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65 70 75	
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80 85 90	
aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr	336
95 100 105 110	
gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile	384
115 120 125	
caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr	432
130 135 140	
acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu	480
145 150 155	
tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His	528
160 165 170	
aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn	576
175 180 185 190	
aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys	624
195 200 205	
ggt ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc Gly Leu Asp Ile Tyr Leu Ile Gly Ile Cys Gly Gly Ser Leu	672
210 215 220	
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225 230 235	
aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His	768
240 245 250	
aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala	816
255 260 265 270	
tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro	864
275 280 285	

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Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His	
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295	300
cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca	960
Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr	
305	310
310	315
caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag	1008
Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln	
320	325
325	330
cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct	1056
Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser	
335	340
340	345
345	350
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Asn	
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25	30
Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe	
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40	45
Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp	
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55	60
Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu	
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70	75
75	80

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Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr  
100 105 110  
Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu  
115 120 125  
Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu  
130 135 140  
Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln  
145 150 155 160  
Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp  
165 170 175  
Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val  
180 185 190  
Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu  
195 200 205  
Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu Leu Met  
210 215 220  
Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln  
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245 250 255  
Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr  
260 265 270  
Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His  
275 280 285  
Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val  
290 295 300  
Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val  
305 310 315 320  
His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys  
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Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe  
15 20 25

tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta  
Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val  
30 35 40 45

cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat  
Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp  
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Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe  
65 70 75

aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac  
Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr  
80 85 90

aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat  
Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn  
95 100 105

att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca  
Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro  
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Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln  
130 135 140

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Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr  
145 150 155

tca tgg gat tgt cct atg gag caa tgt aaa cgt aac tca acc agt ata  
Ser Trp Asp Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile  
160 165 170

tat ttt aag atg gaa aat gat ctt cca caa aaa ata cag tgt act ctt 579

Tyr Phe Lys Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu  
 175 180 185

agc aat cca tta ttt aat aca aca tca tca atc att ttg aca acc tgt 627  
 Ser Asn Pro Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys  
 190 195 200 205

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 Ile Pro Ser Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile  
 210 215 220

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 Pro Leu Ala Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Val Leu  
 225 230 235

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 35 40 45

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Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg  
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Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr  
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Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp  
 100 105 110

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr  
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Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile  
 130 135 140

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp  
145 150 155 160  
Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys  
165 170 175  
Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro  
180 185 190  
Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser  
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<210> 6  
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<220>  
<223> Description of Artificial Sequence: Nucleotide  
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<212> DNA  
<213> Homo sapiens

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<222> (100)...(759)

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Met Leu Arg Leu Leu  
1 5  
ttg gct ctc aac tta ttc cct tca att caa gta aca gga aac aag att 162  
Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val Thr Gly Asn Lys Ile  
10 15 20  
ttg gtg aag cag tcg ccc atg ctt gta gcg tac gac aat ggc gtc aac 210  
Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn Ala Val Asn  
25 30 35  
ctt agc tgc aag tat tcc tac aat ctc ttc tca agg gag ttc cg 258  
Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu Phe Arg Ala  
40 45 50  
tcc ctt cac aaa gga ctg gat agt gct gtg gaa gtc tgt gtt gta tat 306  
Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys Val Val Tyr  
55 60 65  
ggg aat tac tcc cag cag ctt cag gtt tac tca aaa acg ggg ttc aac 354  
Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr Gly Phe Asn  
70 75 80 85  
tgt gat ggg aaa ttg ggc aat gaa tca gtg aca ttc tac ctc cag aat 402  
Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr Leu Gln Asn  
90 95 100  
ttg tat gtt aac caa aca gat att tac ttc tgc aaa att gaa gtt atg 450  
Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile Glu Val Met  
105 110 115  
tat cct cct tac cta gac aat gag aag agc aat gga acc att atc 498  
Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile  
120 125 130  
cat gtg aaa ggg aaa cac ctt tgt cca agt ccc cta ttt ccc gga cct 546  
His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro  
135 140 145  
tct aag ccc ttt tgg gtg ctg gtg gtt ggt gga gtc ctg gct tgc 594  
Ser Lys Pro Phe Trp Val Leu Val Val Gly Gly Val Leu Ala Cys  
150 155 160 165  
tat agc ttg cta gta aca gtg gcc ttt att att ttc tgg gtg agg agt 642  
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser  
170 175 180

aag agg agc agg ctc ctg cac agt gac tac atg aac atg act ccc cgc	690
Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg	
185 190 195	
cgc ccc ggg ccc acc cgc aag cat tac cag ccc tat gcc cca cca cgc	738
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg	
200 205 210	
gac ttc gca gcc tat cgc tcc tgacacggac gcctatccag aagccagccg	789
Asp Phe Ala Ala Tyr Arg Ser	
215 220	
gctggcagcc cccatctgct caatatcact gctctggata gggaaatgacc gccatctcca	849
gccggccacc tcagccctg ttgggccacc aatgccaatt tttctcgagt gactagacca	909
aatatcaaga tcatttttag actctgaaat gaagtaaaag agatttcctg tgacaggcca	969
agtcttacag tgccatggcc cacattccaa cttaccatgt acttagtgac ttgactgaga	1029
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aatacataga cattgtctt tatgaattct gatcatattt agtcattttg accaaatgag	1389
ggatttggtc aaatgagggta ttccctcaaa gcaatatcag gtaaaccaag ttgcttcct	1449
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1514	
agttc	

<210> 8  
 <211> 220  
 <212> PRT  
 <213> Homo sapiens

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20 25 30	
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser	
35 40 45	
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu	

50	55	60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser		
65	70	75
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr		
85	90	95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys		
100	105	110
Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser		
115	120	125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro		
130	135	140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Gly		
145	150	155
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile		
165	170	175
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met		
180	185	190
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro		
195	200	205
Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser		
210	215	220

<210> 9  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

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 gggggccctgg ctgcccaagg taagagcttc ccaggctctc catggccaca gctccggagc 180  
 tctccctgcc ccatgagctc agagcccca gtctgagcca cagcacagcc cccaggaagc 240  
 ggggtgggtg ctgagcggcc tccagtgtct gaggactcat ttaagagaag gaaaaagggt 300  
 ggacccggtg gggagtggcc gggctgtcc aggcagggcc gctgcttgg gaggaagaag 360  
 cccacagtct cggaacacga ggacagcacc tcccccaaca ccacagccgg tgcccagatc 420  
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ccccgtggga gcctccgtca acatcacctg ctccaccaggc gggggcctgc gtgggatcta 660  
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cactacggac agacggttcc ggggcccgt cgaaccttca gggtcccagg acaacctgac 780  
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<210> 10  
<211> 2290  
<212> DNA  
<213> Homo sapiens

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ttgagccccc gtggatcaac gtgctccagg aggactctgt gactctgaca tgccaggggg 180  
ctcgccagccc tgagagcgtac tccattcaat ggttccacaa tggaaatctc attcccaccc 240

acacgcagcc cagctacagg ttcaaggcca acaacaatga cagcggggag tacacgtgcc 300  
agactggcca gaccagcctc agcgaccctg tgcacatgtac tgtgcttcc gaatggctgg 360  
tgctccagac ccctcacctg gagttccagg agggagaaac catcatgctg aggtgccaca 420  
gctggaagga caagcctctg gtcaaggta cattttcca gaatggaaaa tcccagaaat 480  
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tcttctgttc cacatccaca cagccaatac aattagtcaa accactgtta ttaacagatg 2160  
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2290  
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<210> 11  
<211> 1474  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (94)..(984)

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aggccttgg aactcaggag ttttgagagc aaa atg aca aca ccc aga aat tca 114  
Met Thr Thr Pro Arg Asn Ser  
1 5

gta aat ggg act ttc ccg gca gag cca atg aaa ggc cct att gct atg 162  
Val Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met  
10 15 20

caa tct ggt cca aaa cca ctc ttc agg agg atg tct tca ctg gtg ggc 210  
Gln Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Ser Leu Val Gly  
25 30 35

ccc acg caa agc ttc ttc atg agg gaa tct aag act ttg ggg gct gtc 258  
Pro Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val  
40 45 50 55

cag att atg aat ggg ctc ttc cac att gcc ctg ggg ggt ctt ctg atg 306  
Gln Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met  
60 65 70

atc cca gca ggg atc tat gca ccc atc tgt gtg act gtg tgg tac cct 354  
Ile Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro  
75 80 85

ctc tgg gga ggc att atg tat att att tcc gga tca ctc ctg gca gca 402  
Leu Trp Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu Ala Ala  
90 95 100

acg gag aaa aac tcc agg aag tgt ttg gtc aaa gga aaa atg ata atg		450	
Thr Glu Lys Asn Ser Arg Lys Cys Leu Val Lys Gly Lys Met Ile Met			
105	110	115	
aat tca ttg agc ctc ttt gct gcc att tct gga atg att ctt tca atc		498	
Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile			
120	125	130	135
atg gac ata ctt aat att aaa att tcc cat ttt tta aaa atg gag agt		546	
Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser			
140	145	150	
ctg aat ttt att aga gct cac aca cca tat att aac ata tac aac tgt		594	
Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys			
155	160	165	
gaa cca gct aat ccc tct gag aaa aac tcc cca tct acc caa tac tgt		642	
Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys			
170	175	180	
tac agc ata caa tct ctg ttc ttg ggc att ttg tca gtg atg ctg atc		690	
Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile			
185	190	195	
ttt gcc ttc ttc cag gaa ctt gta ata gct ggc atc gtt gag aat gaa		738	
Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu			
200	205	210	215
tgg aaa aga acg tgc tcc aga ccc aaa tct aac ata gtt ctc ctg tca		786	
Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Ser			
220	225	230	
gca gaa gaa aaa aaa gaa cag act att gaa ata aaa gaa gaa gtg gtt		834	
Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val			
235	240	245	
ggg cta act gaa aca tct tcc caa cca aag aat gaa gaa gac att gaa		882	
Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu			
250	255	260	
att att cca atc caa gaa gag gaa gaa gaa aca gag acg aac ttt		930	
Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe			
265	270	275	
cca gaa cct ccc caa gat cag gaa tcc tca cca ata gaa aat gac agc		978	
Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp Ser			
280	285	290	295
tct cct taagtgattt cttctgtttt ctgtttccctt ttttaaacat tagtgttcat		1034	
Ser Pro			
agcttccaag agacatgctg actttcattt cttgaggtac tctgcacata cgaccacat	1094		
ctctatctgg cctttgcattg gagtgaccat agctccttct ctcttacatt gaatgttagag	1154		

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acctgatgga aaagatata gactgctca tgacattcct aaactatctt ttttttattc 1394  
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cttagagca caatggatct 1474

<210> 12  
<211> 297  
<212> PRT  
<213> Homo sapiens

<400> 12  
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20 25 30  
Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu  
35 40 45  
Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile  
50 55 60  
Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile  
65 70 75 80  
Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile  
85 90 95  
Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu  
100 105 110  
Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile  
115 120 125  
Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser  
130 135 140  
His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro  
145 150 155 160  
Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn  
165 170 175  
Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly  
180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile  
195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys  
210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile  
225 230 235 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro  
245 250 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu  
260 265 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser  
275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro  
290 295

<210> 13

<211> 1888

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(1608)

<400> 13

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ctg gtc ctc ggg gct ctg ttc cca gga cct ggc aat gcc cag aca 99  
Leu Val Leu Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr  
15 20 25

tct gtg tcc ccc tca aaa gtc atc ctg ccc cgg gga ggc tcc gtg ctg 147  
Ser Val Ser Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu  
30 35 40 45

gtg aca tgc agc acc tcc tgt gac cag ccc aag ttg ttg ggc ata gag 195  
Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu  
50 55 60

acc ccg ttg cct aaa aag gag ttg ctc ctg cct ggg aac aac cgg aag 243  
Thr Pro Leu Pro Lys Lys Glu Leu Leu Pro Gly Asn Asn Arg Lys  
65 70 75

gtg tat gaa ctg agc aat gtg caa gaa gat agc caa cca atg tgc tat	291
Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr	
80 85 90	
tca aac tgc cct gat ggg cag tca aca gct aaa acc ttc ctc acc gtg	339
Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val	
95 100 105	
tac tgg act cca gaa cgg gta gaa ctc gca ccc ctc ccc tct tgg cag	387
Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln	
110 115 120 125	
cca gtg ggc aag aac ctt acc cta cgc tgc cag gta gag ggt ggg gca	435
Pro Val Gly Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Ala	
130 135 140	
ccc cgg gcc aac ctc acc gta gta ctc cgt ggg gag aag gag ctc	483
Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu	
145 150 155	
aaa cgg gag cca gct gta ggg gag ccc gct gag gtc acg acc acg gta	531
Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Val	
160 165 170	
ctg gtg agg aga gat cac cat gga gcc aat ttc tcg tgc cgc act gaa	579
Leu Val Arg Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu	
175 180 185	
ctg gac ctg cgg ccc caa ggg ctg gag ctg ttt gag aac acc tcg gcc	627
Leu Asp Leu Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala	
190 195 200 205	
ccc tac cag ctc cag acc ttt gtc ctg cca gcg act ccc cca caa ctt	675
Pro Tyr Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu	
210 215 220	
gtc agc ccc cgg gtc cta gag gta gac acg cag ggg acc gta gtc tgt	723
Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys	
225 230 235	
tcc ctg gac ggg ctg ttc cca gtc tcg gag gcc cag gtc cac ctg gca	771
Ser Leu Asp Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala	
240 245 250	
ctg ggg gac cag agg ttg aac ccc aca gtc acc tat ggc aac gac tcc	819
Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser	
255 260 265	
ttc tcg gcc aag gcc tca gtc agt gta acc gca gag gac gag ggc acc	867
Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr	
270 275 280 285	
cag cgg ctg acg tgt gca gta ata ctg ggg aac cag acg cag gag aca	915
Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr	
290 295 300	

ctg cag aca gtg acc atc tac agc ttt ccg gcg ccc aac gtg att ctg Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu 305	310	315	963	
acg aag cca gag gtc tca gaa ggg acc gag gtg aca gtg aag tgt gag Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu 320	325	330	1011	
gcc cac cct aga gcc aag gtg acg ctg aat ggg gtt cca gcc cag cca Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro 335	340	345	1059	
ctg ggc ccg agg gcc cag ctc ctg aag gcc acc cca gag gac aac Leu Gly Pro Arg Ala Gln Leu Leu Lys Ala Thr Pro Glu Asp Asn 350	355	360	365	1107
ggg cgc agc ttc tcc tgc tct gca acc ctg gag gtg gcc ggc cag ctt Gly Arg Ser Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu 370	375	380	1155	
ata cac aag aac cag acc cgg gag ctt cgt gtc ctg tat ggc ccc cga Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg 385	390	395	1203	
ctg gac gag agg gat tgt ccg gga aac tgg acg tgg cca gaa aat tcc Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser 400	405	410	1251	
cag cag act cca atg tgc cag gct tgg ggg aac cca ttg ccc gag ctc Gln Gln Thr Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu 415	420	425	1299	
aag tgt cta aag gat ggc act ttc cca ctg ccc atc ggg gaa tca gtg Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val 430	435	440	445	1347
act gtc act cga gat ctt gag ggc acc tac ctc tgt cgg gcc agg agc Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser 450	455	460	1395	
act caa ggg gag gtc acc cgc gag gtg acc gtg aat gtg ctc tcc ccc Thr Gln Gly Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro 465	470	475	1443	
cgg tat gag att gtc atc atc act gtg gta gca gcc gca gtc ata atg Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Val Ile Met 480	485	490	1491	
ggc act gca ggc ctc agc acg tac ctc tat aac cgc cag cgg aag atc Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile 495	500	505	1539	

<210> 14  
<211> 532  
<212> PRT  
<213> *Homo sapiens*

<400> 14  
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 50 55 60  
 65  
 70 75 80  
 85 90 95  
 100 105 110  
 115 120 125  
 130 135 140  
 145 150 155 160

Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg  
 165 170 175  
 Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu  
 180 185 190  
 Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln  
 195 200 205  
 Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro  
 210 215 220  
 Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp  
 225 230 235 240  
 Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp  
 245 250 255  
 Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala  
 260 265 270  
 Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu  
 275 280 285  
 Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr  
 290 295 300  
 Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro  
 305 310 315 320  
 Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro  
 325 330 335  
 Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro  
 340 345 350  
 Arg Ala Gln Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser  
 355 360 365  
 Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys  
 370 375 380  
 Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu  
 385 390 395 400  
 Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser Gln Gln Thr  
 405 410 415  
 Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu  
 420 425 430  
 Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr  
 435 440 445

Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly  
450 455 460 480

Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu  
465 470 475 480

Ile Val Ile Ile Thr Val Val Ala Ala Ala Val Ile Met Gly Thr Ala  
485 490 495

Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr  
500 505 510

Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro Asn Thr Gln  
515 520 525

Ala Thr Pro Pro  
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<210> 15

<211> 1922

<212> DNA

<213> Homo sapiens

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gctgcagtgc ctcaagggga cctcagatgg ccccaactcg cagctgaccc ggtctcg 180  
gtccccgtt aaacccttct taaaactcag cctggggctg ccaggcctgg gaatccacat 240  
gaggccctg gccatctggc ttttcatctt caacgtctct caacagatgg ggggcttcta 300  
cctgtgccag ccggggccccc cctctgagaa ggcctggcag cctggctgga cagtcataatgt 360  
ggagggcagc ggggagctgt tccggtgaa tgtttggac ctaggtggcc tgggtgtgg 420  
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accgaggac agcctgaacc aggcctcag ccaggaccc accatggccc ctggctccac 600  
actctggctg tcctgtgggg taccgcctga ctctgtgtcc aggggcccccc tctcctggac 660  
ccatgtgcac cccaaaggggc ctaagtcatt gctgagccata gagctgaagg acgatcgccc 720  
ggccagagat atgtggtaa tggagacggg tctgttggc cccggggcca cagctcaaga 780  
cgctggaaag tattattgtc accgtggcaa cctgaccatg tcattccacc tggagatcac 840  
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gactttggct tatctgatct tctgcctgtg ttcccttgc ggcattttc atcttcaaag 960  
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agtgacgcct ccccccaggaa gcggggccca gaaccagtac gggAACGTGc tgtctctccc 1080  
cacacccacc tcaggcctcg gacgcgccc gcgttggcc gcaggcctgg ggggactgc 1140  
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ccgcccggag tggcccaaga agaagaggaa ggggagggtat gaggaacc tgacagttag 1260  
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aatccccatg ggccagaccc agcctggggg ggagggggcc gcatgggcac ctggagcacc 1680  
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gtgcattgtgt gtaagtgtgt gtgtgtgtgt gtgtgtgtat acatgccagt 1860  
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1922  
aa

<210> 16  
<211> 1476  
<212> DNA  
<213> Homo sapiens

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atgggacttt cccggcagag ccaatgaaag gcccatttgc tatgcaatct ggtccaaaac 180  
cactcttca gaggatgtct tcactggtgg gccccacgca aagcttcttc atgaggaaat 240  
ctaagacttt gggggctgtc cagattatga atgggtctt ccacattgcc ctgggggtc 300  
ttctgtatgtat cccagcaggat atctatgcac ccattgtgt gactgtgtgg taccctctct 360

ggggaggcat tatgtatatt attccggat cactcctggc agcaacggag aaaaactcca 420  
ggaagtgttt ggtcaaaagga aaaatgataa tgaattcatt gagcctctt gctgccattt 480  
ctggaatgtat tcttcaatc atggacatac ttaatattaa aatttcccat tttttaaaaa 540  
tggagagtct gaattttatt agagctcaca caccatatac taacatatac aactgtgaac 600  
cagctaattcc ctctgagaaa aactccccat ctacccaata ctgttacagc atacaatctc 660  
tgttcttggg cattttgtca gtatgtca tctttgcctt cttccaggaa cttgtatag 720  
ctggcatcggt tgagaatgaa tgaaaaagaa cgtgctccag acccaaattct aacatagttc 780  
tcctgtcagc agaagaaaaaa aaagaacaga ctattgaaat aaaagaagaa gtggttggc 840  
taactgaaac atcttccaa ccaaagaatg aagaagacat tggaaattttt ccaatccaag 900  
aagaggaaga agaagaaaca gagacgaact ttccagaacc tcccaagat caggaatcct 960  
caccaataga aaatgacagc ttccttaag tgatttcttc tggtttctgt ttcccttttt 1020  
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cacatacgca ccacatctct atctggcctt tgcatggagt gaccatagct cttctctct 1140  
tacattgaat gtagagaatg tagccattgt agcagttgt gttgtcacgc ttcttctttt 1200  
gagcaacttt cttacactga agaaaggcag aatgagtgt tcagaatgtg atttcctact 1260  
aacctgttcc ttggataggc ttttagtat agtattttt ttgtcattt tctccatcag 1320  
caaccaggga gactgcacct gatggaaaag atatatgact gcttcatgac attcctaaac 1380  
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caatgatgca aaaggcttt agagcacaat ggatct 1476

<210> 17  
<211> 2290  
<212> DNA  
<213> Homo sapiens

<400> 17  
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ttgagccccc gtggatcaac gtgctccagg aggactctgt gactctgaca tgccaggggg 180  
ctcgccagccc tgagagcgac tccattcagt gttccacaa tggaaatctc attcccaccc 240  
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agactggcca gaccaggcctc agcgaccctg tgcacatcgac tggctttcc gaatggctgg 360  
tgctccagac ccctcacctg gagttccagg agggagaaac catcatgctg aggtgccaca 420  
gctggaaagga caagcctctg gtcaaggta cattcttca gaatggaaaa tcccagaaat 480  
tctcccgtt gnatcccacc ttctccatcc cacaagcaaa ccacagtcac agtggtgatt 540  
accactgcac aggaaacata ggctacacgc tggtctcatc caagcctgtg accatcaactg 600  
tccaagtgcc cagcatggc agctttcac caatggggat cattgtggct gtggtcattg 660  
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aaatgattgc catcagaaag agacaacttg aagaaaccaa caatgactat gaaacagctg 840  
acggcggcta catgactctg aaccccagg cacctactga cgatgataaa aacatctacc 900  
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ttaaatggag actggaaaaa tcctgagcaa aaaaaaccac ctggccctt gaaatagctt 1080  
taactttgct taaactacaa acacaagcaa aacttcacgg ggtcataacta catacaagca 1140  
taagcaaaac ttaacttggta tcatttctgg taaatgctta tgtagaaat aagacaaccc 1200  
cagccaatca caagcagcct actaacat aatttaggtga cttagggact tctaagaaga 1260  
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ttaagtctcc attgtttgc ctgggattt gagaagagaa ttagagaggt gaggatctgg 1920  
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aggactcttc cagagtcata tacctgagtc ccaaagctcc ctgtcctgaa agccacagac 2040  
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tagcaacatg agaaacgctt atgttacagg ttacatgaga gcaatcatgt aagtctatat 2220  
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2290  
ggtaaaaaaa

<210> 18  
<211> 2171  
<212> DNA  
<213> Homo sapiens

<400> 18  
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tcatatgctt ctgtggacag ctgtgctatc cctggctctt gttgctggg cacctgcagc 180  
tcccccaaag gctgtgctga aactcgagcc ccagtgatc aacgtgctcc aggaggactc 240  
tgtgactctg acatgccggg ggactcacag ccctgagagc gactccattc agtggttcca 300  
caatggaaat ctcattccca cccacacgca gcccagctac aggttcaagg ccaacaacaa 360  
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gactgtgctt tctggtcagt ggaggaaggc cccaggggtgg acctgggagg gccaggacgg 480  
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cagaagaagg tttcaaggcc aaaaacaggc agccaagtgt gagagaagca gaaggaaatc 660  
cctactgcat aaaacccatt tccattttaa tggcagaatt gaaaagcaca gaccacaact 720  
gaatccttagc cctggaaatg actcactata caacatgatg aattcattt acccttgagt 780  
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<210> 19  
<211> 1004  
<212> DNA  
<213> Homo sapiens

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catgcagaga aaaacagttac ctaataaaca gtcagtgtc ttctttgtgc cagccaggac 180  
agaaaactggt gagtgactgc acagagttca ctgaaaacgga atgccttcct tgcggtgaaa 240  
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ccaacctagg gtttcgggtc cagcagaagg gcacccaga aacagacacc atctgcacct 360  
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ccaacactgc tgctccagtg caggagactt tacatggatg ccaaccggtc acccaggagg 840  
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tgtggccacg tgggcaaaca ggcagttggc cagagacctt ggtgctgctg ctgcaggggt 960  
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<210> 20  
<211> 1870  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (211)..(1626)

<400> 20  
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gaaccagagc ttgttagaaac cactttaatc atatccagga gtttgcaaga aacaggtgct 180  
taacactaat tcaccctcctg aacaagaaaa atg ggc tgt gac cgg aac tgt ggg 234  
Met Gly Cys Asp Arg Asn Cys Gly  
1 5

ctc atc gct ggg gct gtc att ggt gct gtc ctg gct gtg ttt gga ggt 282  
Leu Ile Ala Gly Ala Val Ile Gly Ala Val Leu Ala Val Phe Gly Gly  
10 15 20

att cta atg cca gtt gga gac ctg ctt atc cag aag aca att aaa aag 330  
Ile Leu Met Pro Val Gly Asp Leu Leu Ile Gln Lys Thr Ile Lys Lys  
25 30 35 40

caa gtt gtc ctc gaa gaa ggt aca att gct ttt aaa aat tgg gtt aaa 378  
 Gln Val Val Leu Glu Glu Gly Thr Ile Ala Phe Lys Asn Trp Val Lys  
 45 50 55  
 aca ggc aca gaa gtt tac aga cag ttt tgg atc ttt gat gtg caa aat 426  
 Thr Gly Thr Glu Val Tyr Arg Gln Phe Trp Ile Phe Asp Val Gln Asn  
 60 65 70  
 cca cag gaa gtg atg atg aac agc agc aac att caa gtt aag caa aga 474  
 Pro Gln Glu Val Met Met Asn Ser Ser Asn Ile Gln Val Lys Gln Arg  
 75 80 85  
 ggt cct tat acg tac aga gtt cgt ttt cta gcc aag gaa aat gta acc 522  
 Gly Pro Tyr Thr Tyr Arg Val Arg Phe Leu Ala Lys Glu Asn Val Thr  
 90 95 100  
 cag gac gct gag gac aac aca gtc tct ttc ctg cag ccc aat ggt gcc 570  
 Gln Asp Ala Glu Asp Asn Thr Val Ser Phe Leu Gln Pro Asn Gly Ala  
 105 110 115 120  
 atc ttc gaa cct tca cta tca gtt gga aca gag gct gac aac ttc aca 618  
 Ile Phe Glu Pro Ser Leu Ser Val Gly Thr Glu Ala Asp Asn Phe Thr  
 125 130 135  
 gtt ctc aat ctg gct gtg gca gct gca tcc cat atc tat caa aat caa 666  
 Val Leu Asn Leu Ala Val Ala Ala Ser His Ile Tyr Gln Asn Gln  
 140 145 150  
 ttt gtt caa atg atc ctc aat tca ctt att aac aag tca aaa tct tct 714  
 Phe Val Gln Met Ile Leu Asn Ser Leu Ile Asn Lys Ser Lys Ser Ser  
 155 160 165  
 atg ttc caa gtc aga act ttg aga gaa ctg tta tgg ggc tat agg gat 762  
 Met Phe Gln Val Arg Thr Leu Arg Glu Leu Leu Trp Gly Tyr Arg Asp  
 170 175 180  
 cca ttt ttg agt ttg gtt ccg tac cct gtt act acc aca gtt ggt ctg 810  
 Pro Phe Leu Ser Leu Val Pro Tyr Pro Val Thr Thr Val Gly Leu  
 185 190 195 200  
 ttt tat cct tac aac aat act gca gat gga gtt tat aaa gtt ttc aat 858  
 Phe Tyr Pro Tyr Asn Asn Thr Ala Asp Gly Val Tyr Lys Val Phe Asn  
 205 210 215  
 gga aaa gat aac ata agt aaa gtt gcc ata atc gac aca tat aaa ggt 906  
 Gly Lys Asp Asn Ile Ser Lys Val Ala Ile Ile Asp Thr Tyr Lys Gly  
 220 225 230  
 aaa agg aat ctg tcc tat tgg gaa agt cac tgc gac atg att aat ggt 954  
 Lys Arg Asn Leu Ser Tyr Trp Glu Ser His Cys Asp Met Ile Asn Gly  
 235 240 245  
 aca gat gca gcc tca ttt cca cct ttt gtt gag aaa agc cag gta ttg 1002  
 Thr Asp Ala Ala Ser Phe Pro Pro Phe Val Glu Lys Ser Gln Val Leu  
 250 255 260

cag ttc ttt tct tct gat att tgc agg tca atc tat gct gta ttt gaa Gln Phe Phe Ser Ser Asp Ile Cys Arg Ser Ile Tyr Ala Val Phe Glu 265	270	275	280	1050
tcc gac gtt aat ctg aaa gga atc cct gtg tat aga ttt gtt ctt cca Ser Asp Val Asn Leu Lys Gly Ile Pro Val Tyr Arg Phe Val Leu Pro 285	290	295		1098
tcc aag gcc ttt gcc tct cca gtt gaa aac cca gac aac tat tgt ttc Ser Lys Ala Phe Ala Ser Pro Val Glu Asn Pro Asp Asn Tyr Cys Phe 300	305	310		1146
tgc aca gaa aaa att atc tca aaa aat tgt aca tca tat ggt gtg cta Cys Thr Glu Lys Ile Ile Ser Lys Asn Cys Thr Ser Tyr Gly Val Leu 315	320	325		1194
gac atc agc aaa tgc aaa gaa ggg aga cct gtg tac att tca ctt cct Asp Ile Ser Lys Cys Lys Glu Gly Arg Pro Val Tyr Ile Ser Leu Pro 330	335	340		1242
cat ttt ctg tat gca agt cct gat gtt tca gaa cct att gat gga tta His Phe Leu Tyr Ala Ser Pro Asp Val Ser Glu Pro Ile Asp Gly Leu 345	350	355	360	1290
aac cca aat gaa gaa gaa cat agg aca tac ttg gat att gaa cct ata Asn Pro Asn Glu Glu His Arg Thr Tyr Leu Asp Ile Glu Pro Ile 365	370	375		1338
act gga ttc act tta caa ttt gca aaa cgg ctg cag gtc aac cta ttg Thr Gly Phe Thr Leu Gln Phe Ala Lys Arg Leu Gln Val Asn Leu Leu 380	385	390		1386
gtc aag cca tca gaa aaa att caa gta tta aag aat ctg aag agg aac Val Lys Pro Ser Glu Lys Ile Gln Val Leu Lys Asn Leu Lys Arg Asn 395	400	405		1434
tat att gtg cct att ctt tgg ctt aat gag act ggg acc att ggt gat Tyr Ile Val Pro Ile Leu Trp Leu Asn Glu Thr Gly Thr Ile Gly Asp 410	415	420		1482
gag aag gca aac atg ttc aga agt caa gta act gga aaa ata aac ctc Glu Lys Ala Asn Met Phe Arg Ser Gln Val Thr Gly Lys Ile Asn Leu 425	430	435	440	1530
ctt ggc ctg ata gaa atg atc tta ctc agt gtt ggt gtg gtg atg ttt Leu Gly Leu Ile Glu Met Ile Leu Leu Ser Val Gly Val Val Met Phe 445	450	455		1578
gtt gct ttt atg att tca tat tgt gca tgc aga tcg aaa aca ata aaa Val Ala Phe Met Ile Ser Tyr Cys Ala Cys Arg Ser Lys Thr Ile Lys 460	465	470		1626
taagtatgtta ccaaaaaata ttgcttcaat aatatttagct tatataattac ttgtttcac				1686

tttatcaaag agaagttaca tattaggcca tatataattc tagacatgtc tagccactga 1746  
tcattttaa atataggtaa ataaacctat aaatattatc acgcagatca ctaaagtata 1806  
tcttaattc tgggagaaat gagataaaag atgtacttgt gaccattgta acaatagcac 1866  
1870  
aaat

<210> 21  
<211> 472  
<212> PRT  
<213> Homo sapiens

<400> 21  
Met Gly Cys Asp Arg Asn Cys Gly Leu Ile Ala Gly Ala Val Ile Gly  
1 5 10 15  
Ala Val Leu Ala Val Phe Gly Gly Ile Leu Met Pro Val Gly Asp Leu  
20 25 30  
Leu Ile Gln Lys Thr Ile Lys Lys Gln Val Val Leu Glu Glu Gly Thr  
35 40 45  
Ile Ala Phe Lys Asn Trp Val Lys Thr Gly Thr Glu Val Tyr Arg Gln  
50 55 60  
Phe Trp Ile Phe Asp Val Gln Asn Pro Gln Glu Val Met Met Asn Ser  
65 70 75 80  
Ser Asn Ile Gln Val Lys Gln Arg Gly Pro Tyr Thr Tyr Arg Val Arg  
85 90 95  
Phe Leu Ala Lys Glu Asn Val Thr Gln Asp Ala Glu Asp Asn Thr Val  
100 105 110  
Ser Phe Leu Gln Pro Asn Gly Ala Ile Phe Glu Pro Ser Leu Ser Val  
115 120 125  
Gly Thr Glu Ala Asp Asn Phe Thr Val Leu Asn Leu Ala Val Ala Ala  
130 135 140  
Ala Ser His Ile Tyr Gln Asn Gln Phe Val Gln Met Ile Leu Asn Ser  
145 150 155 160  
Leu Ile Asn Lys Ser Lys Ser Ser Met Phe Gln Val Arg Thr Leu Arg  
165 170 175  
Glu Leu Leu Trp Gly Tyr Arg Asp Pro Phe Leu Ser Leu Val Pro Tyr  
180 185 190  
Pro Val Thr Thr Thr Val Gly Leu Phe Tyr Pro Tyr Asn Asn Thr Ala  
195 200 205

Asp Gly Val Tyr Lys Val Phe Asn Gly Lys Asp Asn Ile Ser Lys Val  
210 215 220  
Ala Ile Ile Asp Thr Tyr Lys Gly Lys Arg Asn Leu Ser Tyr Trp Glu  
225 230 235 240  
Ser His Cys Asp Met Ile Asn Gly Thr Asp Ala Ala Ser Phe Pro Pro  
245 250 255  
Phe Val Glu Lys Ser Gln Val Leu Gln Phe Phe Ser Ser Asp Ile Cys  
260 265 270  
Arg Ser Ile Tyr Ala Val Phe Glu Ser Asp Val Asn Leu Lys Gly Ile  
275 280 285  
Pro Val Tyr Arg Phe Val Leu Pro Ser Lys Ala Phe Ala Ser Pro Val  
290 295 300  
Glu Asn Pro Asp Asn Tyr Cys Phe Cys Thr Glu Lys Ile Ile Ser Lys  
305 310 315 320  
Asn Cys Thr Ser Tyr Gly Val Leu Asp Ile Ser Lys Cys Lys Glu Gly  
325 330 335  
Arg Pro Val Tyr Ile Ser Leu Pro His Phe Leu Tyr Ala Ser Pro Asp  
340 345 350  
Val Ser Glu Pro Ile Asp Gly Leu Asn Pro Asn Glu Glu Glu His Arg  
355 360 365  
Thr Tyr Leu Asp Ile Glu Pro Ile Thr Gly Phe Thr Leu Gln Phe Ala  
370 375 380  
Lys Arg Leu Gln Val Asn Leu Leu Val Lys Pro Ser Glu Lys Ile Gln  
385 390 395 400  
Val Leu Lys Asn Leu Lys Arg Asn Tyr Ile Val Pro Ile Leu Trp Leu  
405 410 415  
Asn Glu Thr Gly Thr Ile Gly Asp Glu Lys Ala Asn Met Phe Arg Ser  
420 425 430  
Gln Val Thr Gly Lys Ile Asn Leu Leu Gly Leu Ile Glu Met Ile Leu  
435 440 445  
Leu Ser Val Gly Val Val Met Phe Val Ala Phe Met Ile Ser Tyr Cys  
450 455 460  
Ala Cys Arg Ser Lys Thr Ile Lys  
465 470

<210> 22  
<211> 1321  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> (37)..(1158)

<400> 22 gacagattc actgctcca ccagcttgga gacaac atg tgg ttc ttg aca act 54  
Met Trp Phe Leu Thr Thr  
1 5

ctg ctc ctt tgg gtt cca gtt gat ggg caa gtg gac acc aca aag gca 102  
 Leu Leu Leu Trp Val Pro Val Asp Gly Gln Val Asp Thr Thr Lys Ala  
 10 15 20

gtg atc tct ttg cag cct cca tgg gtc agc gtg ttc caa gag gaa acc 150  
 Val Ile Ser Leu Gln Pro Pro Trp Val Ser Val Phe Gln Glu Glu Thr  
 25 30 35

gta acc ttg cac tgt gag gtg ctc cat ctg cct ggg agc agc tct aca 198  
 Val Thr Leu His Cys Glu Val Leu His Leu Pro Gly Ser Ser Ser Thr  
 40 45 50

cag tgg ttt ctc aat ggc aca gcc act cag acc tcg acc ccc agc tac 246  
 Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln Thr Ser Thr Pro Ser Tyr  
 55 60 65 70

294  
aga atc acc tct gcc agt gtc aat gac agt ggt gaa tac agg tgc cag  
Arg Ile Thr Ser Ala Ser Val Asn Asp Ser Gly Glu Tyr Arg Cys Gln  
75 80 85

342  
 aga ggt ctc tca ggg cga agt gac ccc ata cag ctg gaa atc cac aga  
 Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile Gln Leu Glu Ile His Arg  
 90 95 100

ggc tgg cta cta ctg cag gtc tcc agc aga gtc ttc acg gaa gga gaa 390  
 Gly Trp Leu Leu Leu Gln Val Ser Ser Arg Val Phe Thr Glu Gly Glu  
 105 110 115

cct ctg gcc ttg agg tgt cat gcg tgg aag gat aag ctg gtg tac aat 438  
 Pro Leu Ala Leu Arg Cys His Ala Trp Lys Asp Lys Leu Val Tyr Asn  
 120 125 130

gtg ctt tac tat cga aat ggc aaa gcc ttt aag ttt ttc cac tgg aat 486  
 Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe Lys Phe Phe His Trp Asn  
 135 140 145 150

tct aac ctc acc att ctg aaa acc aac ata agt cac aat ggc acc tac 534  
 Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile Ser His Asn Gly Thr Tyr  
 155 160 165

cat tgc tca ggc atg gga aag cat cgc tac aca tca gca gga ata tct 582

His	Cys	Ser	Gly	Met	Gly	Lys	His	Arg	Tyr	Thr	Ser	Ala	Gly	Ile	Ser	
170							175							180		
gtc act gtg aaa gag cta ttt cca gct cca gtg ctg aat gca tct gtg															630	
Val	Thr	Val	Lys	Glu	Leu	Phe	Pro	Ala	Pro	Val	Leu	Asn	Ala	Ser	Val	
185														195		
aca tcc cca ctc ctg gag ggg aat ctg gtc acc ctg agc tgt gaa aca															678	
Thr	Ser	Pro	Leu	Leu	Glu	Gly	Asn	Leu	Val	Thr	Leu	Ser	Cys	Glu	Thr	
200														210		
aag ttg ctc ttg cag agg cct ggt ttg cag ctt tac ttc tcc ttc tac															726	
Lys	Leu	Leu	Gln	Arg	Pro	Gly	Leu	Gln	Leu	Tyr	Phe	Ser	Phe	Tyr		
215														230		
atg ggc agc aag acc ctg cga ggc agg aac aca tcc tct gaa tac caa															774	
Met	Gly	Ser	Lys	Thr	Leu	Arg	Gly	Arg	Asn	Thr	Ser	Ser	Glu	Tyr	Gln	
235														245		
ata cta act gct aga aga gaa gac tct ggg tta tac tgg tgc gag gct															822	
Ile	Leu	Thr	Ala	Arg	Arg	Glu	Asp	Ser	Gly	Leu	Tyr	Trp	Cys	Glu	Ala	
250														260		
gcc aca gag gat gga aat gtc ctt aag cgc agc cct gag ttg gag ctt															870	
Ala	Thr	Glu	Asp	Gly	Asn	Val	Leu	Lys	Arg	Ser	Pro	Glu	Leu	Glu	Leu	
265														275		
caa gtg ctt ggc ctc cag tta cca act cct gtc tgg ttt cat gtc ctt															918	
Gln	Val	Leu	Gly	Leu	Gln	Leu	Pro	Thr	Pro	Val	Trp	Phe	His	Val	Leu	
280														290		
ttc tat ctg gca gtg gga ata atg ttt tta gtg aac act gtt ctc tgg															966	
Phe	Tyr	Leu	Ala	Val	Gly	Ile	Met	Phe	Leu	Val	Asn	Thr	Val	Ile	Trp	
295														305		
gtg aca ata cgt aaa gaa ctg aaa aga aag aaa aag tgg gat tta gaa															1014	
Val	Thr	Ile	Arg	Lys	Glu	Leu	Lys	Arg	Lys	Lys	Trp	Asp	Leu	Glu		
														325		
315																
atc tct ttg gat tct ggt cat gag aag gta act tcc agc ctt caa															1062	
Ile	Ser	Leu	Asp	Ser	Gly	His	Glu	Lys	Lys	Val	Thr	Ser	Ser	Leu	Gln	
330														340		
gaa gac aga cat tta gaa gaa gag ctg aaa tgt cag gaa caa aaa gaa															1110	
Glu	Asp	Arg	His	Leu	Glu	Glu	Leu	Lys	Cys	Gln	Glu	Gln	Lys	Glu		
345														355		
gaa cag ctg cag gaa ggg gtg cac cgg aag gag ccc cag ggg gcc acg															1158	
Glu	Gln	Leu	Gln	Glu	Gly	Val	His	Arg	Lys	Glu	Pro	Gln	Gly	Ala	Thr	
360														370		
tagcagcggc tcagtgggtg gccatcgatc tggaccgtcc cctgcccact tgctccccgt															1218	
gaggactgct tacaaacatc caaaaagttca acaacaccag aactgtgtgt ctcatggtat															1278	

gtaactctta aagcaaataa atgaactgac ttcaaaaaaa aaa

1321

<210> 23  
<211> 374  
<212> PRT  
<213> Homo sapiens

<400> 23  
Met Trp Phe Leu Thr Thr Leu Leu Leu Trp Val Pro Val Asp Gly Gln  
1 5 10 15  
Val Asp Thr Thr Lys Ala Val Ile Ser Leu Gln Pro Pro Trp Val Ser  
20 25 30  
Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu  
35 40 45  
Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln  
50 55 60  
Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser  
65 70 75 80  
Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile  
85 90 95  
Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg  
100 105 110  
Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys  
115 120 125  
Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe  
130 135 140  
Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile  
145 150 155 160  
Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr  
165 170 175  
Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro  
180 185 190  
Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val  
195 200 205  
Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln  
210 215 220  
Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn  
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly  
 245 250 255  
 Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg  
 260 265 270  
 Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro  
 275 280 285  
 Val Trp Phe His Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu  
 290 295 300  
 Val Asn Thr Val Leu Trp Val Thr Ile Arg Lys Glu Leu Lys Arg Lys  
 305 310 315 320  
 Lys Lys Trp Asp Leu Glu Ile Ser Leu Asp Ser Gly His Glu Lys Lys  
 325 330 335  
 Val Thr Ser Ser Leu Gln Glu Asp Arg His Leu Glu Glu Glu Leu Lys  
 340 345 350  
 Cys Gln Glu Gln Lys Glu Glu Gln Leu Gln Glu Gly Val His Arg Lys  
 355 360 365  
 Glu Pro Gln Gly Ala Thr  
 370

<210> 24  
 <211> 1714  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (156)..(1163)

<400> 24  
 gcggggagct tgcatgacc aagagggtgt tgaggctagg aggccacgat aaacaggata 60  
 cgataaaagt ccttaaccaa gacgcagatg ggaagaagcg ttagagcgag cagcactcac 120  
 atctcaagaa ccagccttcc aaacagtttc cagag atg gat tat cct act tta 173  
 Met Asp Tyr Pro Thr Leu  
 1 5

ctt ttg gct ctt cat gta tac aga gct cta tgt gaa gag gtg ctt 221  
 Leu Leu Ala Leu Leu His Val Tyr Arg Ala Leu Cys Glu Val Leu  
 10 15 20

tgg cat aca tca gtt ccc ttt gcc gag aac atg tct cta gaa tgt gtg 269  
 Trp His Thr Ser Val Pro Phe Ala Glu Asn Met Ser Leu Glu Cys Val  
 25 30 35

tat cca tca atg ggc atc tta aca cag gtg gag tgg ttc aag atc ggg Tyr Pro Ser Met Gly Ile Leu Thr Gln Val Glu Trp Phe Lys Ile Gly 40 45 50	317
acc cag cag gat tcc ata gcc att ttc agc cct act cat ggc atg gtc Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser Pro Thr His Gly Met Val 55 60 65 70	365
ata agg aag ccc tat gct gag agg gtt tac ttt ttg aat tca acg atg Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr Phe Leu Asn Ser Thr Met 75 80 85	413
gct tcc aat aac atg act ctt ttc ttt cgg aat gcc tct gaa gat gat Ala Ser Asn Asn Met Thr Leu Phe Phe Arg Asn Ala Ser Glu Asp Asp 90 95 100	461
gtt ggc tac tat tcc tgc tct ctt tac act tac cca cag gga act tgg Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr Tyr Pro Gln Gly Thr Trp 105 110 115	509
cag aag gtg ata cag gtg gtt cag tca gat agt ttt gag gca gct gtg Gln Lys Val Ile Gln Val Gln Ser Asp Ser Phe Glu Ala Ala Val 120 125 130	557
cca tca aat agc cac att gtt tcg gaa cct gga aag aat gtc aca ctc Pro Ser Asn Ser His Ile Val Ser Glu Pro Gly Lys Asn Val Thr Leu 135 140 145 150	605
act tgt cag cct cag atg acg tgg cct gtg cag gca gtg agg tgg gaa Thr Cys Gln Pro Gln Met Thr Trp Pro Val Gln Ala Val Arg Trp Glu 155 160 165	653
aag atc cag ccc cgt cag atc gac ctc tta act tac tgc aac ttg gtc Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu Thr Tyr Cys Asn Leu Val 170 175 180	701
cat ggc aga aat ttc acc tcc aag ttc cca aga caa ata gtg agc aac His Gly Arg Asn Phe Thr Ser Lys Phe Pro Arg Gln Ile Val Ser Asn 185 190 195	749
tgc agc cac gga agg tgg agc gtc atc gtc atc ccc gat gtc aca gtc Cys Ser His Gly Arg Trp Ser Val Ile Val Ile Pro Asp Val Thr Val 200 205 210	797
tca gac tcg ggg ctt tac cgc tgc tac ttg cag gcc agc gca gga gaa Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu Gln Ala Ser Ala Gly Glu 215 220 225 230	845
aac gaa acc ttc gtg atg aga ttg act gta gcc gag ggt aaa acc gat Asn Glu Thr Phe Val Met Arg Leu Thr Val Ala Glu Gly Lys Thr Asp 235 240 245	893
aac caa tat acc ctc ttt gtg gct gga ggg aca gtt tta ttg ttg ttg Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly Thr Val Leu Leu Leu 250 255 260	941

ttt gtt atc tca att acc acc atc att gtc att ttc ctt aac aga agg	989
Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg	
265 270 275	
aga agg aga gag aga aga gat cta ttt aca gag tcc tgg gat aca cag	1037
Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln	
280 285 290	
aag gca ccc aat aac tat aga agt ccc atc tct acc ggt caa cct acc	1085
Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Gly Gln Pro Thr	
295 300 305 310	
aat caa tcc atg gat gat aca aga gag gat att tat gtc aac tat cca	1133
Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro	
315 320 325	
acc ttc tct cgc aga cca aag act aga gtt taagcttatt ct tgacatga	1183
Thr Phe Ser Arg Arg Pro Lys Thr Arg Val	
330 335	
gtgcattagt aatgactttt atgtactcat gcatggatct ttatgcaatt tttttccact	1243
acccaaggc taccttagat actagttgtc tgaattgagt tactttgata gaaaaatac	1303
ttcattacct aaaatcattt ttcatagaac tgtttcagaa aacctgactc taactggttt	1363
atatacaaaa gaaaacttac ttttatcatat aacagaatga tccaggggag attaagctt	1423
ggcaaggc tatattaccag ggcttaaatg ttgtgtctag aattaagtat gggcataaac	1483
tggcttctga atccctttcc agagtttgg atccatttcc ctggcttgg ctcactctc	1543
atgcaggctt tcctcttgc ttggcaagat ggctgccaac tcttggcaat tcatacatcc	1603
ttgtttctgt ctggtagaga gtttgcttct caaatggagc aaacaaattt gattatttt	1663
tcattgttaa ataggcaaca tgaccataaa ggttggatg gcttaagtaa a	1714

<210> 25  
 <211> 336  
 <212> PRT  
 <213> Homo sapiens

<400> 25	
Met Asp Tyr Pro Thr Leu Leu Leu Ala Leu Leu His Val Tyr Arg Ala	
1 5 10 15	
Leu Cys Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn	
20 25 30	
Met Ser Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val	
35 40 45	

Glu Trp Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser  
 50 55 60  
 Pro Thr His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr  
 65 70 75 80  
 Phe Leu Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg  
 85 90 95  
 Asn Ala Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr  
 100 105 110  
 Tyr Pro Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp  
 115 120 125  
 Ser Phe Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro  
 130 135 140  
 Gly Lys Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val  
 145 150 155 160  
 Gln Ala Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu  
 165 170 175  
 Thr Tyr Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro  
 180 185 190  
 Arg Gln Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val  
 195 200 205  
 Ile Pro Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu  
 210 215 220  
 Gln Ala Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val  
 225 230 235 240  
 Ala Glu Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly  
 245 250 255  
 Thr Val Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val  
 260 265 270  
 Ile Phe Leu Asn Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr  
 275 280 285  
 Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile  
 290 295 300  
 Ser Thr Gly Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp  
 305 310 315 320  
 Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val  
 325 330 335

<210> 26  
<211> 2107  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (35)..(1975)

<400> 26  
acgcggaaac aggcttgcac ccagacacga cacc atg cat ctc ctc ggc ccc tgg 55  
Met His Leu Leu Gly Pro Trp  
1 5

ctc ctg ctc ctg gtt cta gaa tac ttg gct ttc tct gac tca agt aaa 103  
Leu Leu Leu Leu Val Leu Glu Tyr Leu Ala Phe Ser Asp Ser Ser Lys  
10 15 20

tgg gtt ttt gag cac cct gaa acc ctc tac gcc tgg gag ggg gcc tgc 151  
Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp Glu Gly Ala Cys  
25 30 35

gtc tgg atc ccc tgc acc tac aga gcc cta gat ggt gac ctg gaa agc 199  
Val Trp Ile Pro Cys Thr Tyr Arg Ala Leu Asp Gly Asp Leu Glu Ser  
40 45 50 55

ttc atc ctg ttc cac aat cct gag tat aac aag aac acc tcg aag ttt 247  
Phe Ile Leu Phe His Asn Pro Glu Tyr Asn Lys Asn Thr Ser Lys Phe  
60 65 70

gat ggg aca aga ctc tat gaa agc aca aag gat ggg aag gtt cct tct 295  
Asp Gly Thr Arg Leu Tyr Glu Ser Thr Lys Asp Gly Lys Val Pro Ser  
75 80 85

gag cag aaa agg gtg caa ttc ctg gga gac aag aat aag aac tgc aca 343  
Glu Gln Lys Arg Val Gln Phe Leu Gly Asp Lys Asn Lys Asn Cys Thr  
90 95 100

ctg agt atc cac ccg gtg cac ctc aat gac agt ggt cag ctg ggg ctg 391  
Leu Ser Ile His Pro Val His Leu Asn Asp Ser Gly Gln Leu Gly Leu  
105 110 115

agg atg gag tcc aag act gag aaa tgg atg gaa cga ata cac ctc aat 439  
Arg Met Glu Ser Lys Thr Glu Lys Trp Met Glu Arg Ile His Leu Asn  
120 125 130 135

gtc tct gaa agg cct ttt cca cct cat atc cag ctc cct cca gaa att 487  
Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Leu Pro Pro Glu Ile  
140 145 150

caa gag tcc cag gaa gtc act ctg acc tgc ttg ctg aat ttc tcc tgc 535  
Gln Glu Ser Gln Glu Val Thr Leu Thr Cys Leu Leu Asn Phe Ser Cys  
155 160 165

tat ggg tat ccg atc caa ttg cag tgg ctc cta gag ggg gtt cca atg Tyr Gly Tyr Pro Ile Gln Leu Gln Trp Leu Leu Glu Gly Val Pro Met 170 175 180	583
agg cag gct gtc acc tcg acc tcc ttg acc atc aag tct gtc ttc Arg Gln Ala Ala Val Thr Ser Thr Ser Leu Thr Ile Lys Ser Val Phe 185 190 195	631
acc cgg agc gag ctc aag ttc tcc cca cag tgg agt cac cat ggg aag Thr Arg Ser Glu Leu Lys Phe Ser Pro Gln Trp Ser His His Gly Lys 200 205 210 215	679
att gtg acc tgc cag ctt cag gat gca gat ggg aag ttc ctc tcc aat Ile Val Thr Cys Gln Leu Gln Asp Ala Asp Gly Lys Phe Leu Ser Asn 220 225 230	727
gac acg gtg cag ctg aac gtg aag cat cct ccc aag aag gtg acc aca Asp Thr Val Gln Leu Asn Val Lys His Pro Pro Lys Lys Val Thr Thr 235 240 245	775
gtg att caa aac ccc atg ccg att cga gaa gga gac aca gtg acc ctt Val Ile Gln Asn Pro Met Pro Ile Arg Glu Gly Asp Thr Val Thr Leu 250 255 260	823
tcc tgt aac tac aat tcc agt aac ccc agt gtt acc cgg tat gaa tgg Ser Cys Asn Tyr Asn Ser Ser Asn Pro Ser Val Thr Arg Tyr Glu Trp 265 270 275	871
aaa ccc cat ggc gcc tgg gag gag cca tcg ctt ggg gtg ctg aag atc Lys Pro His Gly Ala Trp Glu Glu Pro Ser Leu Gly Val Leu Lys Ile 280 285 290 295	919
caa aac gtt ggc tgg gac aac aca acc atc gcc tgc gca gct tgt aat Gln Asn Val Gly Trp Asp Asn Thr Thr Ile Ala Cys Ala Ala Cys Asn 300 305 310	967
agt tgg tgc tcg tgg gcc tcc cct gtc gcc ctg aat gtc cag tat gcc Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu Asn Val Gln Tyr Ala 315 320 325	1015
ccc cga gac gtg agg gtc cgg aaa atc aag ccc ctt tcc gag att cac Pro Arg Asp Val Arg Val Lys Ile Lys Pro Leu Ser Glu Ile His 330 335 340	1063
tct gga aac tcg gtc agc ctc caa tgt gac ttc tca agc agc cac ccc Ser Gly Asn Ser Val Ser Leu Gln Cys Asp Phe Ser Ser Ser His Pro 345 350 355	1111
aaa gaa gtc cag ttc ttc tgg gag aaa aat ggc agg ctt ctg ggg aaa Lys Glu Val Gln Phe Phe Trp Glu Lys Asn Gly Arg Leu Leu Gly Lys 360 365 370 375	1159
gaa agc cag ctg aat ttt gac tcc atc tcc cca gaa gat gct ggg agt Glu Ser Gln Leu Asn Phe Asp Ser Ile Ser Pro Glu Asp Ala Gly Ser 380 385 390	1207

tac agc tgc tgg gtg aac aac tcc ata gga cag aca gcg tcc aag gcc Tyr Ser Cys Trp Val Asn Asn Ser Ile Gly Gln Thr Ala Ser Lys Ala 395	400	405	1255	
tgg aca ctt gaa gtg ctg tat gca ccc agg agg ctg cgt gtg tcc atg Trp Thr Leu Glu Val Leu Tyr Ala Pro Arg Arg Leu Arg Val Ser Met 410	415	420	1303	
agc ccg ggg gac caa gtg atg gag ggg aag agt gca acc ctg acc tgt Ser Pro Gly Asp Gln Val Met Glu Gly Lys Ser Ala Thr Leu Thr Cys 425	430	435	1351	
gag agc gac gcc aac cct ccc gtc tcc cac tac acc tgg ttt gac tgg Glu Ser Asp Ala Asn Pro Pro Val Ser His Tyr Thr Trp Phe Asp Trp 440	445	450	455	1399
aat aac caa agc ctc ccc tac cac agc cag aag ctg aga ttg gag ccg Asn Asn Gln Ser Leu Pro Tyr His Ser Gln Lys Leu Arg Leu Glu Pro 460	465	470	1447	
gtg aag gtc cag cac tcg ggt gcc tac tgg tgc cag ggg acc aac agt Val Lys Val Gln His Ser Gly Ala Tyr Trp Cys Gln Gly Thr Asn Ser 475	480	485	1495	
gtg ggc aag ggc cgt tcg cct ctc agc acc ctc acc gtc tac tat agc Val Gly Lys Gly Arg Ser Pro Leu Ser Thr Leu Thr Val Tyr Tyr Ser 490	495	500	1543	
ccg gag acc atc ggc agg cga gtg gct gtg gga ctc ggg tcc tgc ctc Pro Glu Thr Ile Gly Arg Val Ala Val Gly Leu Gly Ser Cys Leu 505	510	515	1591	
gcc atc ctc atc ctg gca atc tgt ggg ctc aag ctc cag cga cgt tgg Ala Ile Leu Ile Ala Ile Cys Gly Leu Lys Leu Gln Arg Arg Trp 520	525	530	535	1639
aag agg aca cag agc cag cag ggg ctt cag gag aat tcc agc ggc cag Lys Arg Thr Gln Ser Gln Gln Gly Leu Gln Glu Asn Ser Ser Gly Gln 540	545	550	1687	
agc ttc ttt gtg agg aat aaa aag gtt aga agg gcc ccc ctc tct gaa Ser Phe Phe Val Arg Asn Lys Lys Val Arg Arg Ala Pro Leu Ser Glu 555	560	565	1735	
ggc ccc cac tcc ctg gga tgc tac aat cca atg atg gaa gat ggc att Gly Pro His Ser Leu Gly Cys Tyr Asn Pro Met Met Glu Asp Gly Ile 570	575	580	1783	
agc tac acc acc ctg cgc ttt ccc gag atg aac ata cca cga act gga Ser Tyr Thr Thr Leu Arg Phe Pro Glu Met Asn Ile Pro Arg Thr Gly 585	590	595	1831	

gat gca gag tcc tca gag atg cag aga cct ccc ccg gac tgc gat gac	1879
Asp Ala Glu Ser Ser Glu Met Gln Arg Pro Pro Pro Asp Cys Asp Asp	
600 605 610 615	
acg gtc act tat tca gca ttg cac aag cgc caa gtg ggc act atg aga	1927
Thr Val Thr Tyr Ser Ala Leu His Lys Arg Gln Val Gly Thr Met Arg	
620 625 630	
acg tca ttc cag att ttc cag aag atg agg gga ttc att act cag agc	1975
Thr Ser Phe Gln Ile Phe Gln Lys Met Arg Gly Phe Ile Thr Gln Ser	
635 640 645	
tgatccagtt tgggtcgaa gagcggcctc aggcacaaga aaatgtggac tatgtgatcc	2035
tcaaacattg acactggatg ggctgcagca gaggcactgg gggcagcggg ggccaggaa	2095
gtccccgagt tt	2107

<210> 27  
 <211> 647  
 <212> PRT  
 <213> Homo sapiens

<400> 27	
Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu	
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Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu	
20 25 30	
Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala	
35 40 45	
Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr	
50 55 60	
Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr	
65 70 75 80	
Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly	
85 90 95	
Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn	
100 105 110	
Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp	
115 120 125	
Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His	
130 135 140	
Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr	
145 150 155 160	

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp  
 165 170 175  
 Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser  
 180 185 190  
 Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro  
 195 200 205  
 Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala  
 210 215 220  
 Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His  
 225 230 235 240  
 Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg  
 245 250 255  
 Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro  
 260 265 270  
 Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro  
 275 280 285  
 Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr  
 290 295 300  
 Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val  
 305 310 315 320  
 Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys Ile  
 325 330 335  
 Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln Cys  
 340 345 350  
 Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu Lys  
 355 360 365  
 Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser Ile  
 370 375 380  
 Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser Ile  
 385 390 395 400  
 Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala Pro  
 405 410 415  
 Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu Gly  
 420 425 430  
 Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val Ser  
 435 440 445

His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His Ser  
 450 455 460  
 Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala Tyr  
 465 470 475 480  
 Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu Ser  
 485 490 495  
 Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val Ala  
 500 505 510  
 Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys Gly  
 515 520 525  
 Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu  
 530 535 540  
 Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val  
 545 550 555 560  
 Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn  
 565 570 575  
 Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu  
 580 585 590  
 Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg  
 595 600 605  
 Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His Lys  
 610 615 620  
 Arg Gln Val Gly Thr Met Arg Thr Ser Phe Gln Ile Phe Gln Lys Met  
 625 630 635 640  
 Arg Gly Phe Ile Thr Gln Ser  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (101)..(880)

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 cagcaactgg gcacagaaag gagccgcctg ggcaggacc atg gca cgg cca cat 115  
 Met Ala Arg Pro His  
 1 5

ccc tgg tgg ctg tgc gtt ctg ggg acc ctg gtg ggg ctc tca gct act	163
Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val Gly Leu Ser Ala Thr	
10	15
20	
cca gcc ccc aag agc tgc cca gag agg cac tac tgg gct cag gga aag	211
Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr Trp Ala Gln Gly Lys	
25	30
35	
ctg tgc tgc cag atg tgt gag cca gga aca ttc ctc gtg aag gac tgt	259
Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe Leu Val Lys Asp Cys	
40	45
50	
gac cag cat aga aag gct gct cag tgt gat cct tgc ata ccg ggg gtc	307
Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro Cys Ile Pro Gly Val	
55	60
65	
tcc ttc tct cct gac cac acc cgg ccc cac tgt gag agc tgt cgg	355
Ser Phe Ser Pro Asp His His Thr Arg Pro His Cys Glu Ser Cys Arg	
70	75
80	85
cac tgt aac tct ggt ctt ctc gtt cgc aac tgc acc atc act gcc aat	403
His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys Thr Ile Thr Ala Asn	
90	95
100	
gct gag tgt gcc tgt cgc aat ggc tgg cag tgc agg gac aag gag tgc	451
Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys Arg Asp Lys Glu Cys	
105	110
115	
acc gag tgt gat cct ctt cca aac cct tcg ctg acc gct cgg tcg tct	499
Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu Thr Ala Arg Ser Ser	
120	125
130	
cag gcc ctg agc cca cac cct cag ccc acc cac tta cct tat gtc agt	547
Gln Ala Leu Ser Pro His Pro Gln Pro Thr His Leu Pro Tyr Val Ser	
135	140
145	
gag atg ctg gag gcc agg aca gct ggg cac atg cag act ctg gct gac	595
Glu Met Leu Glu Ala Arg Thr Ala Gly His Met Gln Thr Leu Ala Asp	
150	155
160	165
ttc agg cag ctg cct gcc cgg act ctc tct acc cac tgg cca ccc caa	643
Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr His Trp Pro Pro Gln	
170	175
180	
aga tcc ctg tgc agc tcc gat ttt att cgc atc ctt gtg atc ttc tct	691
Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile Leu Val Ile Phe Ser	
185	190
195	
gga atg ttc ctt gtt ttc acc ctg gcc ggg gcc ctg ttc ctc cat caa	739
Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala Leu Phe Leu His Gln	
200	205
210	

cga agg aaa tat aga tca aac aaa gga gaa agt cct gtg gag cct gca	787
Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro Ala	
215 220 225	
gag cct tgt cgt tac agc tgc ccc agg gag gag gag ggc agc acc atc	835
Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu Gly Ser Thr Ile	
230 235 240 245	
ccc atc cag gag gat tac cga aaa ccg gag cct gcc tgc tcc ccc	880
Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro	
250 255 260	
tgagccagca cctgcggtag ctgcactaca gccctggcct ccaccccccac cccgcccacc 940	
atccaaggga gagtgagacc tggcagccac aactgcagtc ccattcctttt gtcagggccc 1000	
tttcctgtgt acacgtgaca gagtgccttt tcgagactgg cagggacgag gacaaatatg 1060	
gatgaggtgg agagtggaa gcaggagccc agccagctgc gcctgcgctg caggagggcg 1120	
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aaaataaaagt gacagatgac c	1201

<210> 29  
 <211> 260  
 <212> PRT  
 <213> Homo sapiens

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Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr	
20 25 30	
Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe	
35 40 45	
Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro	
50 55 60	
Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His	
65 70 75 80	
Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys	
85 90 95	
Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys	
100 105 110	
Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu	
115 120 125	

Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His  
 130 135 140  
 Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met  
 145 150 155 160  
 Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr  
 165 170 175  
 His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile  
 180 185 190  
 Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala  
 195 200 205  
 Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser  
 210 215 220  
 Pro Val Glu Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu  
 225 230 235 240  
 Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro  
 245 250 255  
 Ala Cys Ser Pro  
 260

<210> 30  
 <211> 2350  
 <212> DNA  
 <213> Homo sapiens

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 aagaactaga gaaggaccaa gcaaagccat gatatttcca tggaaatgtc agagcaccca 120  
 gagggactta tggaaacatct tcaagttgtg ggggtggaca atgctctgtt gtgatttcct 180  
 ggcacatcat ggaaccgact gctggactta ccattattct gaaaaaccca tgaactggca 240  
 aagggctaga agattctgcc gagacaattha cacagattta gttgccatac aaaacaaggc 300  
 gaaaatttag tatctggaga agactctgcc tttcagtcgt tcttactact ggataggaat 360  
 ccggaagata ggaggaatat ggacgtgggt gggacccaac aaatctctca ctgaagaagc 420  
 agagaactgg ggagatggtg agcccaaccaa caagaagaac aaggaggact gcgtggagat 480  
 ctatatcaag agaaacaaag atgcaggcaa atgaaacgt gacgcctgcc acaaactaaa 540  
 ggcagccctc tgttacacag cttcttgcca gccctggtca tgcagtggcc atggagaatg 600  
 tgttagaaatc atcaataatt acacctgcaa ctgtgatgtg gggtactatg ggccccagtg 660

tcagttgtg attcagtgtg agccttgga ggccccagag ctgggtacca tggactgtac 720  
tcactcttg ggaaacttca gcttcagctc acagtgtgcc tttagctgct ctgaaggaac 780  
aaacttaact gggattgaag aaaccacctg tggaccattt ggaaactggt catctccaga 840  
accaacctgt caagtgattc agtgtgagcc tctatcagca ccagatttg ggatcatgaa 900  
ctgtagccat cccctggcca gcttcagctt tacctctgca tgtaccttca tctgctcaga 960  
aggaactgag ttaattggga agaagaaaac catttgcgaa tcatctggaa tctggtc当地 1020  
tccttagtcca atatgtcaaa aattggacaa aagtttctca atgattaagg agggtgatta 1080  
taaccccttc ttcattccag tggcagtcgat ggttactgca ttctctgggt tggcatttat 1140  
catttggctg gcaaggagat taaaaaaagg caagaaatcc aagagaagta tgaatgaccc 1200  
atattaaatc gcccctgggt aaagaaaatt cttggaaatac taaaaatcat gagatcctt 1260  
aaatccttcc atgaaacgtt ttgtgtgggt gcacccctca cgtcaaacat gaagtgtgtt 1320  
tccttcagtg catctggaa gatttctacc tgaccaacag ttcccttcagc ttccatttcg 1380  
cccctcattt atccctcaac ccccaagccca caggtgttta tacagctcag cttttgcct 1440  
tttctgagga gaaacaaata agaccataaa gggaaaggat tcatgtggaa tataaagatg 1500  
gctgactttg ctcttccttg actcttgcgtt tcagttcaa ttcaatgtgctg tacttgatga 1560  
cagacacttc taaatgaagt gcaaatttga tacatatgtg aatatggact cagtttctt 1620  
gcagatcaaa ttccacgtcg tcttcgttat actgtggagg tacactcttta tagaaagttc 1680  
aaaaagtcta cgcttcctt tctttcttaac tccagtgaaat gaaatgggtc ctgctcaagt 1740  
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tggcttcagc ctccccaccc tcttcagcca cctctttt tcagttggct gacttccaca 1860  
cttagcatct catgagtgcc aagcaaaaagg agagaagaga gaaatgcct gcgctgttt 1920  
tttttttttta tcacgatatt attagtaaga aaacatcaact gaaatgcttag ctgcaagtga 2040  
catcttttg atgtcatatg gaagagttaa aacaggtgga gaaattccctt gattcacaat 2100  
gaaatgctctt cctttccctt gccccccagac cttttatccg acttacccat attctacata 2160  
ttcttttaat ttcatctcag gcctccctca accccaccac ttctttata acttagtcctt 2220  
tactaatcca acccatgatg agtccttctt cctggcttct tactgaaagg ttaccctgta 2280

acatgcaatt ttgcatttga ataaagcctg ctttttaagt gttaaaaaaaaaaa 2340  
 2350  
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<210> 31  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (116)..(1198)

<400> 31  
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 cggccaggga tcctccagct ccttcgccc gcgcctccg ttcgctccgg acacc atg 118  
 Met  
 1

gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166  
 gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg  
 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu  
 5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214  
 agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta  
 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val  
 20 25 30

ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262  
 ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc  
 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala  
 35 40 45

gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310  
 gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag  
 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln  
 50 55 60 65

atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358  
 atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc  
 Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe  
 70 75 80

ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt 406  
 ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt  
 Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys  
 85 90 95

gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag 454  
 gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag  
 Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln  
 100 105 110

tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt 502  
 tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt  
 Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys  
 115 120 125

aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata	550
Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile	
130 135 140 145	
act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac	598
Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr	
150 155 160	
aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac	646
Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp	
165 170 175	
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac	694
Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr	
180 185 190	
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt	742
Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser	
195 200 205	
ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa	790
Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln	
210 215 220 225	
gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gaa tct gaa	838
Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser Glu	
230 235 240	
tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc	886
Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Ala Asn Thr Thr	
245 250 255	
tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ttg	934
Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu	
260 265 270	
gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt tgc att gca gtc	982
Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val	
275 280 285	
aac agt cga aga agg tgt ggg cag aag aaa aag cta gtg atc aac agt	1030
Asn Ser Arg Arg Cys Gly Gln Lys Lys Leu Val Ile Asn Ser	
290 295 300 305	
ggc aat gga gct gtg gag gac aga aag cca agt gga ctc aac gga gag	1078
Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu	
310 315 320	
gcc agc aag tct cag gaa atg gtg cat ttg gtg aac aag gag tcg tca	1126
Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser	
325 330 335	
gaa act cca gac cag ttt atg aca gct gat gag aca agg aac ctg cag	1174
Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln	
340 345 350	

aat gtg gac atg aag att ggg gtg taacacccatc accattatct tggaaagaaa 1228  
Asn Val Asp Met Lys Ile Gly Val  
355 360

caaccgttgtt aaacataacc attacaggga gctggacac ttaacagatg caatgtgcta 1288  
ctgattgttt cattgcgaat ctttttagc ataaaatttt ctactcttt tgttaaaaaa 1348  
aaaaaaaaa 1354

<210> 32  
<211> 361  
<212> PRT  
<213> Homo sapiens

<400> 32  
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Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly  
20 25 30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu  
35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala  
50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly  
65 70 75 80

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile  
85 90 95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser  
100 105 110

Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Asp  
115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr  
130 135 140

Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu  
145 150 155 160

Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp  
165 170 175

Asp Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly  
180 185 190

Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp  
195 200 205  
Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp  
210 215 220  
Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser  
225 230 235 240  
Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr  
245 250 255  
Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile  
260 265 270  
Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala  
275 280 285  
Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn  
290 295 300  
Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly  
305 310 315 320  
Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser  
325 330 335  
Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu  
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Gln Asn Val Asp Met Lys Ile Gly Val  
355 360

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<212> DNA  
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<220>  
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<222> (116)..(1594)

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Met  
1

gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166  
Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu  
5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val	214
20 25 30	
ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala	262
35 40 45	
gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln	310
50 55 60 65	
atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe	358
70 75 80	
ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys	406
85 90 95	
gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln	454
100 105 110	
tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys	502
115 120 125	
aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile	550
130 135 140 145	
act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr	598
150 155 160	
aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp	646
165 170 175	
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr	694
180 185 190	
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser	742
195 200 205	
ccc tgg atc acc gac agc aca gac aga atc cct cgt acc aat atg gac Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met Asp	790
210 215 220 225	
tcc agt cat agt aca acg ctt cag cct act gca aat cca aac aca ggt Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly	838
230 235 240	

ttg gtg gaa gat ttg gac agg aca gga cct ctt tca atg aca acg cag	886		
Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr Gln			
245	250	255	
cag agt aat tct cag agc ttc tct aca tca cat gaa ggc ttg gaa gaa	934		
Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu Glu			
260	265	270	
gat aaa gac cat cca aca act tct act ctg aca tca agc aat agg aat	982		
Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn			
275	280	285	
gat gtc aca ggt gga aga aga gac cca aat cat tct gaa ggc tca act	1030		
Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser Thr			
290	295	300	305
cat tta ctg gaa ggt tat acc tct cat tac cca cac acg aag gaa agc	1078		
His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu Ser			
310	315	320	
agg acc ttc atc cca gtg acc tca gct aag act ggg tcc ttt gga gtt	1126		
Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly Val			
325	330	335	
act gca gtt act gtt gga gat tcc aac tct aat gtc aat cgt tcc tta	1174		
Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser Leu			
340	345	350	
tca gga gac caa gac aca ttc cac ccc agt ggg ggg tcc cat acc act	1222		
Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr			
355	360	365	
cat gga tct gaa tca gat gga cac tca cat ggg agt caa gaa ggt gga	1270		
His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly			
370	375	380	385
gca aac aca acc tct ggt cct ata agg aca ccc caa att cca gaa tgg	1318		
Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp			
390	395	400	
ctg atc atc ttg gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt	1366		
Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Ile Leu Ala Val			
405	410	415	
tgc att gca gtc aac agt cga aga agg tgt ggg cag aag aaa aag cta	1414		
Cys Ile Ala Val Asn Ser Arg Arg Cys Gly Gln Lys Lys Lys Leu			
420	425	430	
gtg atc aac agt ggc aat gga gct gtg gag gac aga aag cca agt gga	1462		
Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly			
435	440	445	

ctc aac gga gag gcc agc aag tct cag gaa atg gtg cat ttg gtg aac 1510  
 Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn  
 450 455 460 465  
 aag gag tcg tca gaa act cca gac cag ttt atg aca gct gat gag aca 1558  
 Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr  
 470 475 480  
 agg aac ctg cag aat gtg gac atg aag att ggg gtg taacacctac 1604  
 Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val  
 485 490  
 accattatct tggaaagaaa caacgttgg aacataacca ttacagggga gctgggacac 1664  
 ttaacagatg caatgtgcta ctgattgttt catttcgaat ctataatgc ataaaatttt 1724  
 ctactctttt tgttttttgt gttttgttct ttaaagtca gtcacatgg taaaaacagc 1784  
 attgctttct gaaatttaggg cccaattaaat aatcagcaag aattttgatc gtttcagttc 1844  
 cccacttgga ggcctttcat ccctcggtt tgctatggat ggcttctaac aaaaacctac 1904  
 cacatagttt ttcctgatcg ccaaccttgc ccccccaccag ctaaggacat ttccagggtt 1964  
 aatagggcct ggtcctggga ggaaatttga atgggtcatt ttgccttcc attagcctaa 2024  
 tccctggca ttgctttcca ctgagggtgg gggttgggt gtactagttt cacatcttca 2084  
 acagaccccc tctagaaattt ttcagatgc ttctggaga cacccaaagg gtaagtctat 2144  
 ttatctgttag taaaactattt atctgtgttt ttgaaatattt aaaccctgga tcagtccttt 2204  
 tattcagttt aatttttaa agttacttgc tcagaggcac aaaaagggtt taaaactgatt 2264  
 cataataat atctgtaccc tcttcgaaaa aaaaaaaaaa aaaa 2308

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 <211> 493  
 <212> PRT  
 <213> Homo sapiens

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 Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu 35 40 45  
 Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala 50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly  
65 70 75 80  
Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile  
85 90 95  
Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser  
100 105 110  
Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp  
115 120 125  
Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr  
130 135 140  
Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu  
145 150 155 160  
Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp  
165 170 175  
Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly  
180 185 190  
Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp  
195 200 205  
Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met  
210 215 220  
Asp Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr  
225 230 235 240  
Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr  
245 250 255  
Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu  
260 265 270  
Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg  
275 280 285  
Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser  
290 295 300  
Thr His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu  
305 310 315 320  
Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly  
325 330 335  
Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser  
340 345 350

Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr  
355 360 365

Thr His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly  
370 375 380

Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu  
385 390 395 400

Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala  
405 410 415

Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys  
420 425 430

Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser  
435 440 445

Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val  
450 455 460

Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu  
465 470 475 480

Thr Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val  
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<210> 35

<211> 1452

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(730)

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agaatatcac ggc atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc 109  
Met Gly Met Ser Ser Leu Lys Leu Lys Tyr Val  
1 5 10

ctg ttt ttc ttc aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg 157  
Leu Phe Phe Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu  
15 20 25

ggc ttt ggg atc tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc 205  
Gly Phe Gly Ile Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe  
30 35 40

cat aac ctc ccc tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc 253  
His Asn Leu Pro Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly  
45 50 55 60

tct att atc atg gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag Ser Ile Ile Met Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys	301
65 70 75	
gaa aac aag tgt ctg ctt atg tcg ttc atc ctg ctg ctg att atc Glu Asn Lys Cys Leu Leu Met Ser Phe Phe Ile Leu Leu Ile Ile	349
80 85 90	
ctc ctt gct gag gtg acc ttg gcc atc ctg ctc ttt gta tat gaa cag Leu Leu Ala Glu Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln	397
95 100 105	
aag ctg aat gag tat gtg gct aag ggt ctg acc gac agc atc cac cgt Lys Leu Asn Glu Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg	445
110 115 120	
tac cac tca gac aat agc acc aag gca gcg tgg gac tcc atc cag tca Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser	493
125 130 135 140	
ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg acc agt ggc Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly	541
145 150 155	
cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt tgc tat gcg Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala	589
160 165 170	
aaa gca aga ctg tgg ttt cat tcc aat ttc ctg tat atc gga atc atc Lys Ala Arg Leu Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile	637
175 180 185	
acc atc tgt gta tgt gtg att gag gtg ttg ggg atg tcc ttt gca ctg Thr Ile Cys Val Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu	685
190 195 200	
acc ctg aac tgc cag att gac aaa acc agc cag acc ata ggg cta Thr Leu Asn Cys Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu	730
205 210 215	
tgatctgcag tagttctgtg gtgaagagac ttgtttcatc tccggaaatg caaaaccatt 790	
tatagcatga agccctacat gatcactgca ggtatgatcct cctcccatcc tttccctttt 850	
taggtccctg tcttatacaa ccagagaagt ggggtttggc caggcacatc ccatctcagg 910	
cagcaagaca atctttcact cactgacggc agcagccatg tctctcaaag tgggtgaaact 970	
aatatctgag catcttttag acaagagagg caaagacaaa ctggattaa tggcccaaca 1030	
tcaaagggtg aaccaggat atgaattttt gcatctcccc attgtcgaat tagtctccag 1090	
cctctaaata atgcccagtc ttctcccaa agtcaagcaa gagactagtt gaaggagtt 1150	

ctggggccag gctcactgga ccattgtcac aaccctctgt ttctcttga ctaagtgcc 1210  
tggctacagg aattacacag ttctcttct ccaaaggca agatctcatt tcaatttctt 1270  
tattagaggg ccttattgtat gtgttctaag tctttcaga aaaaaactat ccagtgattt 1330  
atatcctgat ttcaaccagt cacttagctg ataattcacag taagaagact tctggattt 1390  
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tt  
1452

<210> 36  
<211> 219  
<212> PRT  
<213> Homo sapiens

<400> 36  
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20 25 30  
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro  
35 40 45  
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met  
50 55 60  
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys  
65 70 75 80  
Leu Leu Met Ser Phe Phe Ile Leu Leu Ile Ile Leu Leu Ala Glu  
85 90 95  
Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln Lys Leu Asn Glu  
100 105 110  
Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg Tyr His Ser Asp  
115 120 125  
Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser Phe Leu Gln Cys  
130 135 140  
Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly Pro Pro Ala Ser  
145 150 155 160  
Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala Lys Ala Arg Leu  
165 170 175  
Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile Thr Ile Cys Val  
180 185 190

Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu Thr Leu Asn Cys  
195 200 205

Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu  
210 215

<210> 37  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide primer

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